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FIGURE 23

Figure 23A

								Section 1
	(1)	1	10	20	30	40	51	
CUR2-1.6.1_HC	(1)	EVQLVESGGGLVVKPGGSLRLSCAASGTFNR					YNHNWVROAPGRGLEWVSSI	
VH3-21	(1)	EVQLVESGGGLVVKPGGSLRLSCAASGTFES					YSMNNWVROAPGRGLEWVSSI	
Consensus	(1)	EVQLVESGGGLVVKPGGSLRLSCAASGF					F SY MNWVROAPGRGLEWVSSI	
								Section 2
	(52)	52	60	70	80	90	102	
CUR2-1.6.1_HC	(52)	SSSSSNLYADSVKGRFTISRDNARNSLYLQMNSLRAEDTAVYYCARDIMI						
VH3-21	(52)	SSSSSVLYYADSVKGRFTISRDNARNSLYLQMNSLRAEDTAVYYCAR----						
Consensus	(52)	SSSSS IYYADSVKGRFTISRDNARNSLYLQMNSLRAEDTAVYYCAR						
								Section 3
	(103)	103	110	126				
CUR2-1.6.1_HC	(103)	TFGGIIASFYFDYWGQGLTVTVSS				SEQ ID NO:13		
VH3-21	(99)	-----				SEQ ID NO:3		
Consensus	(103)							

Figure 23B

								Section 1
	(1)	1	10	20	30	40	51	
CUR2-1.6.1 LC	(1)	DIQMTQSPSSLSASVGDRTITCRASQGI					RNDLGW	QQKPGKAPKRLIYAA
A30	(1)	DIQMTQSPSSLSASVGDRTITCRASQGI					RNDLGW	QQKPGKAPKRLIYAA
Consensus	(1)	DIQMTQSPSSLSASVGDRTITCRASQGI					RNDLGW	FQQKPGKAPKRLIYAA
								Section 2
	(52)	52	60	70	80	90	102	
CUR2-1.6.1 LC	(52)	SSLQSGVPSRPSGSGSGTEFTLTIS						SSLQPEDPATYYCLQHNNSYPLTPGGGT
A30	(52)	SSLQSGVPSRPSGSGSGTEFTLTIS						SSLQPEDPATYYCLQHNNSYP-----
Consensus	(52)	SSLQSGVPSRPSGSGSGTEFTLTIS						SSLQPEDPATYYCLQHNNSYP
								Section 3
	(103)	103	107					
CUR2-1.6.1 LC	(103)	KVEIK		SEQ ID NO:14				
A30	(96)	-----		SEQ ID NO:11				
Consensus	(103)							



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FIGURE 24

Figure 24A

Section 1						
	(1)	10	20	30	40	51
Cur2-1.11.1 HC	(1)	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI				
VH3-53	(1)	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI				
Consensus	(1)	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI				
Section 2						
	(52)	60	70	80	90	102
Cur2-1.11.1 HC	(52)	YSGGSTYYADSVKGRFTISRDN SKNTLYLQMSLPAEDTAVYYCAGTVTTN				
VH3-53	(52)	YSGGSTYYADSVKGRFTISRDN SKNTLYLQMSLPAEDTAVYYCAR-----				
Consensus	(52)	YSGGSTYYADSVKGRFTISRDN SKNTLYLQMSLRAEDTAVYYCA				
Section 3						
	(103)	103	110	120		
Cur2-1.11.1 HC	(103)	YYYGMDVWGQGTTVTVSS			SEQ ID NO:15	
VH3-53	(98)	-----			SEQ ID NO:5	
Consensus	(103)					

Figure 24B

Section 1						
	(1)	10	20	30	40	51
CUR2-1.11.1 LC	(1)	DIVMTQSPLSLPVTPGEPASISCRSSQBLHQNGYNYLDWYLQKPGQSPQQL				
A19	(1)	DIVMTQSPLSLPVTPGEPASISCRSSQSLHNSGYNYLDWYLQKPGQSPQQL				
Consensus	(1)	DIVMTQSPLSLPVTPGEPASISCRSSQSLHNSGYNYLDWYLQKPGQSPQQL				
Section 2						
	(52)	60	70	80	90	102
CUR2-1.11.1 LC	(52)	LIYLGSNRASGVPRDFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTLTP				
A19	(52)	LIYLGSNRASGVPRDFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP--				
Consensus	(52)	LIYLGSNRASGVPRDFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTLT				
Section 3						
	(103)	103	111			
CUR2-1.11.1 LC	(103)	GGGTRVEIK	SEQ ID NO:16			
A19	(101)	-----	SEQ ID NO:8			
Consensus	(103)					



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FIGURE 25

Figure 25A

								Section 1
	(1)	1	10	20	30	40	51	
CR2-1.17.1_HC	(1)	QVQLVESGGGVVQPG SL RLSCAASGFTPS SY GMHWVROAPGKGLEWVAVI						
VH3-33	(1)	QVQLVESGGGVVQPG SL RLSCAASGFTPS SY GMHWVROAPGKGLEWVAVI						
Consensus	(1)	QVQLVESGGGVVQPGK SL RLSCAASGFTPS SY GMHWVROAPGKGLEWVAVI						
								Section 2
	(52)	52	60	70	80	90	102	
CR2-1.17.1_HC	(52)	WYDGSNKYYADSVKGRFTISRDN SKNTLY LQMNSLR AEDTAVYYC ARDQGY						
VH3-33	(52)	WYDGSNKYYADSVKGRFTISRDN SKNTLY LQMNSLR AEDTAVYYC AR----						
Consensus	(52)	WYDGSNKYYADSVKGRFTISRDN SKNTLY LQMNSLR AEDTAVYYC AR						
								Section 3
	(103)	103	110	126				
CR2-1.17.1_HC	(103)	RYAGYYYDYGMDVWGQGT TVTVSS			SEQ ID NO:17			
VH3-33	(99)	-----			SEQ ID NO:4			
Consensus	(103)							

Figure 25B

								Section 1	
	(1)	1	10	20	30	40	52		
CR2-1.17.1 LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI RNDLGWYQ KPGKAPKRLIYAAS							
A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI RNDLGWYQ KPGKAPKRLIYAAS							
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI RNDLGWYQ KPGKAPKRLIYAAS							
								Section 2	
	(53)	53	60	70	80	90	104		
CR2-1.17.1 LC	(53)	SLQSGV PSRFSGSGSGTEFT LTIS SLQPEDPATYYC LQHN SYPLT FGGGTKV							
A30	(53)	SLQSGV PSRFSGSGSGTEFT LTIS SLQPEDPATYYC LQHN SYPLT FGGGTKV							
Consensus	(53)	SLQSGV PSRFSGSGSGTEFT LTIS SLQPEDPATYYC LQHN SYPLT FGGGTKV							
								Section 3	
	(105)	1057							
CR2-1.17.1 LC	(105)	EIK SEQ ID NO:18							
A30	(96)	--- SEQ ID NO:11							
Consensus	(105)								



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FIGURE 26

Figure 26A

Section 1										
	(1)	10	20	30	40	52				
CR2-1.18_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN								
VH1-8	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN								
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN								
Section 2										
	(53)	60	70	80	90	104				
CR2-1.18_HC	(53)	PNSGNTGYAQRFGQGVMTMTRNTSISTAYMELSSLRSEDYAVYYCAPEGIAVA								
VH1-8	(53)	PNSGNTGYAQRFGQGVMTMTRNTSISTAYMELSSLRSEDYAVYYCAR-----								
Consensus	(53)	PNSGNTGYAQRFGQGVMTMTRNTSISTAYMELSSLRSEDYAVYYCAR								
Section 3										
	(105)	105	110	126						
CR2-1.18_HC	(105)	GTYYYYYGMDVWGQGTITVTVSS				SEQ ID NO:19				
VH1-8	(99)	-----				SEQ ID NO:1				
Consensus	(105)									

Figure 26B

Section 1									
	(1)	1	10	20	30	40	50	53	
CR2-1.18_LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLGWYQQRPGKAPKRLIYAASS							
A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLGWYQQRPGKAPKRLIYAASS							
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLGWYQQRPGKAPKRLIYAASS							
Section 2									
	(54)	54	60	70	80	90	100	106	
CR2-1.18_LC	(54)	LQSGVPSRFSGSGSGTEFTLTITSSLPEDPATYFCLQHNSYPFTFGPGTKVDI							
A30	(54)	LQSGVPSRFSGSGSGTEFTLTITSSLPEDPATYFCLQHNSYP-----							
Consensus	(54)	LQSGVPSRFSGSGSGTEFTLTITSSLPEDPATYFCLQHNSYP							
Section 3									
	(107)	107	117	127					
CR2-1.18_LC	(107)	K	SEQ ID NO:20						
A30	(96)	-	SEQ ID NO:11						
Consensus	(107)								



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FIGURE 27

Figure 27A

Section 1									
(1)	1	10	20	30	40	50	60	70	80
Cur2-1.19.1_hc	(1)	QVQLVQSGAEVRRKPGASVKVSCKASGYTF	THYDINWVRQATGQGLEWMGWMN						
VH1-8	(1)	QVQLVQSGAEVRRKPGASVKVSCKASGYTF	THYDINWVRQATGQGLEWMGWMN						
Consensus	(1)	QVQLVQSGAEVRRKPGASVKVSCKASGYTF	THYDINWVRQATGQGLEWMGWMN						
Section 2									
(53)	53	60	70	80	90	100	110	120	130
Cur2-1.19.1_hc	(53)	PNSGNTGYAQKFGGRVTMTRNTSISTAYMEL	SSLRSED	TAVYYC	ARDVMITP				
VH1-8	(53)	PNSGNTGYAQKFGGRVTMTRNTSISTAYMEL	SSLRSED	TAVYYC	ARDVMITP				
Consensus	(53)	PNSGNTGYAQKFGGRVTMTRNTSISTAYMEL	SSLRSED	TAVYYC	ARDVMITP				
Section 3									
(105)	105	110	120	130	140	150	160	170	180
Cur2-1.19.1_hc	(105)	GGVIVHYGMDVWGQGT	TVTVSS						
VH1-8	(99)	-----	-----						
Consensus	(105)	GGVIVHYGMDVWGQGT	TVTVSS						

Figure 27B

Section 1									
(1)	1	10	20	30	40	50	60	70	80
Cur2-1.19.1_lc	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI	RNDLGWYQKPGKAPKRLIYAAS						
A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI	RNDLGWYQKPGKAPKRLIYAAS						
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI	RNDLGWYQKPGKAPKRLIYAAS						
Section 2									
(53)	53	60	70	80	90	100	110	120	130
Cur2-1.19.1_lc	(53)	SLQSGVPSRPFGSGSGT	FTLTIS	SLQPEDPATYYC	LQHN	SDPC	SPGQGT	KL	
A30	(53)	SLQSGVPSRPFGSGSGT	FTLTIS	SLQPEDPATYYC	LQHN	SDPC	SPGQGT	KL	
Consensus	(53)	SLQSGVPSRPFGSGSGT	FTLTIS	SLQPEDPATYYC	LQHN	SDPC	SPGQGT	KL	
Section 3									
(105)	105	110	120	130	140	150	160	170	180
Cur2-1.19.1_lc	(105)	EIR							
A30	(96)	---							
Consensus	(105)	EIR							



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FIGURE 28

Figure 28A

		Section 1					
		(1)	1	10	20	30	40 51
Cur2-1.23.1 HC	(1)	EVQLVQSGAEVKKPGESLRISCEGSGYSPFTSYWIGNVLRQMPGKGLWMMGII					
VH5-51	(1)	EVQLVQSGAEVKKPGESLRISCKGSGYSPFTSYWIGNVLRQMPGKGLWMMGII					
Consensus	(1)	EVQLVQSGAEVKKPGESLRISCGSGYSPFTSYWIGNVLRQMPGKGLWMMGII					
		Section 2					
		(52)	52	60	70	80	90 102
Cur2-1.23.1 HC	(52)	YPGDSDTTRYSPSFQGGVTTISADKSIISTAYLQWSSLRASDTAMYYCARHVS					
VH5-51	(52)	YPGDSDTTRYSPSFQGGVTTISADKSIISTAYLQWSSLRASDTAMYYCAR----					
Consensus	(52)	YPGDSDTTRYSPSFQGGVTTISADKSIISTAYLQWSSLRASDTAMYYCAR					
		Section 3					
		(103)	103	110	126		
Cur2-1.23.1 HC	(103)	YYVSGSYYNVFDYWGQGLVTVSS				SEQ ID NO:23	
VH5-51	(99)	-----				SEQ ID NO:6	
Consensus	(103)						

Figure 28B

							Section 1	
		(1)	1	10	20	30	40	51
Cur2-1.23.1 LC	(1)	DIQMTQSPFSSLSASVGDRVTITCRASQGISIRNDLGWYQQKPGKAPKRLIYAA						
A30	(1)	DIQMTQSPFSSLSASVGDRVTITCRASQGISIRNDLGWYQQKPGKAPKRLIYAA						
Consensus	(1)	DIQMTQSPFSSLSASVGDRVTITCRASQGISIRNDLGWYQQPGKAPKRLIYAA						
							Section 2	
		(52)	52	60	70	80	90	102
Cur2-1.23.1 LC	(52)	SSLQSGVPSPRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPWTFGQGT						
A30	(52)	SSLQSGVPSPRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYP-----						
Consensus	(52)	SSLQSGVPSPRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYP						
							Section 3	
		(103)	103	107				
Cur2-1.23.1 LC	(103)	RVEIK		SEQ ID NO:24				
A30	(96)	-----		SEQ ID NO:11				
Consensus	(103)							



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FIGURE 29

Figure 29A

Section 1							
	(1)	1	10	20	30	40	51
CR2-1.24.1_HC	(1)	QVQLVESGGGVVQPGSRSLRLSCAASGFPSSYGMHWVROAPGKGLEWVADI					
VH3-33	(1)	QVQLVESGGGVVQPGSRSLRLSCAASGFPSSYGMHWVROAPGKGLEWVAVI					
Consensus	(1)	QVQLVESGGGVVQPGSRSLRLSCAASGFPSSYGMHWVROAPGKGLEWVA I					
Section 2							
	(52)	52	60	70	80	90	102
CR2-1.24.1_HC	(52)	WYDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQGY					
VH3-33	(52)	WYDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR----					
Consensus	(52)	WYDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR					
Section 3							
	(103)	103	110	126			
CR2-1.24.1_HC	(103)	SYGYVYYDYGMDVWGQGTITVTVSS			SEQ ID NO:25		
VH3-33	(99)	-----			SEQ ID NO:4		
Consensus	(103)						

Figure 29B

								Section 1			
	(1)	1	10	20	30	40	52				
CR2-1.24.1 LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI RNDLGWYQQRPGKAPKRLIYAAS									
A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI RNDLGWYQQRPGKAPKRLIYAAS									
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI RNDLGWYQQRPGKAPKRLIYAAS									
								Section 2			
	(53)	53	60	70	80	90	104				
CR2-1.24.1 LC	(53)	SLQSGVPSRFSGSGSGTEFTLTISLQPEDPATYYCLOHNSYEWTFGQGTKV									
A30	(53)	SLQSGVPSRFSGSGSGTEFTLTISLQPEDPATYYCLOHNSYP-----									
Consensus	(53)	SLQSGVPSRFSGSGSGTEFTLTISLQPEDPATYYCLOHNSYP									
								Section 3			
	(105)	1067									
CR2-1.24.1 LC	(105)	EIK	SEQ ID NO:26								
A30	(96)	---	SEQ ID NO:11								
Consensus	(105)										



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FIGURE 30

Figure 30A

								Section 1	
	(1)	1	10	20	30	40	51		
VH5-51	(1)	EVQLVQSGAEVKKRPGESLKISCKGSGYSPTSYWIGWVRQMPGKGLEWMGII							
CR2-1.25.1_HC	(1)	EVQLVQSGAEVKKRPGESLKISCKGSGYRPTSYWIGWVRQMPGKGLEWMGII							
Consensus	(1)	EVQLVQSGAEVKKRPGESLKISCKGSGY PTSYWIGWVRQMPGKGLEWMGII							
								Section 2	
	(52)	52	60	70	80	90	102		
VH5-51	(52)	YPGDSDDTRYSPSFQGGVTTISADKSIISTAYLQWSSLKASDTAMYYCAR----							
CR2-1.25.1_HC	(52)	YPGDSDDTRYSPSFQGGVTTISADKSIISTAYLQWSSLKASDTAMYYCARHGSY							
Consensus	(52)	YPGDSDDTRYSPSFQGGVTTISADKSIISTAYLQWSSLKASDTAMYYCAR							
								Section 3	
	(103)	103	110	126					
VH5-51	(99)	-----				SEQ ID NO:6			
CR2-1.25.1_HC	(103)	YYGSETYYNVFDYWGGTLVTVSS				SEQ ID NO:27			
Consensus	(103)								

Figure 30B

								Section 1	
	(1)	1	10	20	30	40	52		
A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIIRNDLGWYQOKPGKAPKRLIYAAS							
CR2-1.25.1_LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIIRNDLGWYQOKPGKAPKRLIYAAS							
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIIRNDLGWYQOKPGKAPKRLIYAAS							
								Section 2	
	(53)	53	60	70	80	90	104		
A30	(53)	SLQSGVPSRFSGSGSGTEFTLTISISLQPEDFATYYCLQHNSYP-----							
CR2-1.25.1_LC	(53)	SLQSGVPSRFSGSGSGTEFTLTISISLQPEDFATYYCLQHNSYRWTFGQGTKV							
Consensus	(53)	SLQSGVPSRFSGSGSGTEFTLTISISLQPEDFATYYCLQHNSYP							
								Section 3	
	(105)	1087							
A30	(96)	---	SEQ ID NO:11						
CR2-1.25.1_LC	(105)	EIK	SEQ ID NO:28						
Consensus	(105)								

		Section 1				
	(1)	10	20	30	40	53
A19	(1)	DIVMTQSLSLPVTPEGPASISCRSSQSLLHNSGYN YLDWYLQKPGQSPQLLI				
CR2-1.29_LC	(1)	DIVMTQSLSLPVTPEGPASISCRSSQSLLHNSGYN YLDWYLQKPGQSPQLLI				
Consensus	(1)	DIVMTQSLSLPVTPEGPASISCRSSQSLLHNSGYN YLDWYLQKPGQSPQLLI				
		Section 2				
	(54)	60	70	80	90	106
A19	(54)	YLGSNRASGVPRDRFSGSGSGTDFTLKISRVEA DVG VVYCMQALQSP-----				
CR2-1.29_LC	(54)	YLGSNRASGVPRDRFSGSGSGTDFTLKISRVEA DVG VVYCMQALQLMCSFGQ				
Consensus	(54)	YLGSNRASGVPRDRFSGSGSGTDFTLKISRVEADDVG VVYCMQALQS				
		Section 3				
	(107)	107	113			
A19	(101)	-----		SEQ ID NO:8		
CR2-1.29_LC	(107)	GTKLEIK		SEQ ID NO:30		
Consensus	(107)					



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FIGURE 32

Figure 32A

								Section 1
	(1)	1	10	20	30	40	52	
VH1-18	(1)	QVQLVQSGAEVRRPGASVKVSCFASGYTFSTSYGTSNWROAPGGGLEWMGWIS						
CR2-1.33_HC	(1)	QVQLVQSGAEVRRPGASVKVSCFASGYTFSTSYGTSNWROAPGGGLEWMGWIS						
Consensus	(1)	QVQLVQSGAEVRRPGASVKVSCFASGYTFSTSYGTSNWROAPGGGLEWMGWIS						
								Section 2
	(53)	53	60	70	80	90	104	
VH1-18	(53)	AYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR-----						
CR2-1.33_HC	(53)	AYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDHYIDS						
Consensus	(53)	AYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR						
								Section 3
	(105)	105	110	127				
VH1-18	(99)	-----			SEQ ID NO:2			
CR2-1.33_HC	(105)	SDYLYYYGLDVWGQGTTVTVSS			SEQ ID NO:31			
Consensus	(105)							

Figure 32B

								Section 1
	(1)	1	10	20	30	40	53	
A20	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQRPGKVPKLLIYAAS						
CR2-1.33_LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQRPGKVPKLLIYAAS						
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQRPGKVPKLLIYAAS						
								Section 2
	(54)	54	60	70	80	90	106	
A20	(54)	LQSGVPSRFSGSGSGTDFTLTITISLQPEDVATYYCQKYNAP-----						
CR2-1.33_LC	(54)	LQSGVPSRFSGSGSGTDFTLTITISLQPEDVATYYCQKYNAPLTPGGGTVKVEI						
Consensus	(54)	LQSGVPSRFSGSGSGTDFTLTITISLQPEDVATYYCQKYNAP						
								Section 3
	(107)	107						
A20	(96)	-					SEQ ID NO:9	
CR2-1.33_LC	(107)	K					SEQ ID NO:32	
Consensus	(107)							

Section 1

	(1)	10	20	30	40	52
A20	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQRPGKVPRLIIYAAS				
CR2-1.38.1_LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQRPGKVPRLIIYAAS				
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQRPGKVP LIIYAAS				

Section 2

	(53)	60	70	80	90	104
A20	(53)	TLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKNSAP-----				
CR2-1.38.1_LC	(53)	TLQSGVPSRFSGSGSGTDFTLTISSLQPEDVAATYQCKNSAPWTFGGQTTV				
Consensus	(53)	TLQSGVPSRFSGSGSGTDFTLTISSLQPEDVA YYCQK NSAP				

Section 3

	(105)	1067	
A20	(96)	---	SEQ ID NO:9
CR2-1.38.1_LC	(105)	EIK	SEQ ID NO:34
Consensus	(105)		



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FIGURE 34

Figure 34A

		Section 1				
	(1)	1	10	20	30	40 51
VH5-51	(1)	EVQLVQSGAEVRRKPGESLKISCKGSGYSPTSYWIGWVRMPGKGLEWMGII				
CR2-1.39.1_HC	(1)	EVQLVQSGTEVRRKPGESLKISCKGSGYRFTSYWIGWVRMPGKGLEWMGII				
Consensus	(1)	EVQLVQSG EVRRKPGESLKISCKGSGY FTSYWIGWVRMPGKGLEWMGII				
		Section 2				
	(52)	52	60	70	80	90 102
VH5-51	(52)	YPGDSDDTRYSPSPQGGVTLISADKSIISTAYLQWSSLKASDTAMYICAR----				
CR2-1.39.1_HC	(52)	YPGDSDDTRYSPSPQGGVTLISADKSIISTAYLQWSSLKASDTAMYICARHGSI				
Consensus	(52)	YPGDSDDTRYSPSPQGGVTLISADKSIISTAYLQWSSLKASDTAMYICAR				
		Section 3				
	(103)	103	110	126		
VH5-51	(99)	-----				SEQ ID NO:6
CR2-1.39.1_HC	(103)	YYNSGSIYNVFDYWGQGLVTVSS				SEQ ID NO:35
Consensus	(103)					

Figure 34B

		Section 1				
	(1)	1	10	20	30	40 52
A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLGWYQQKPKGAPKRLIYAAS				
CR2-1.39.1_LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLGWYQQKPKGAPKRLIYAAS				
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLGWYQQKPKGAPKRLIYAAS				
		Section 2				
	(53)	53	60	70	80	90 104
A30	(53)	SLQSGVPDRFSGSGSGTEFTLTISGLPEDFATYYCLOHNSYP-----				
CR2-1.39.1_LC	(53)	SLQSGVPDRFSGSGSGTEFTLTISGLPEDFATYYCLOHNSYPWTFPGQGTKV				
Consensus	(53)	SLQSGVPDRFSGSGSGTEFTLTISGLPEDFATYYCLOHNSYP				
		Section 3				
	(105)	105	1067			
A30	(96)	---				SEQ ID NO:11
CR2-1.39.1_LC	(105)	EIK				SEQ ID NO:36
Consensus	(105)					

							Section 1
	(1)	10	20	30	40	53	
A20	(1)	DIQMTQSP PSLS ASVGD RV ITCRASQGISNYLAWYCQKPGKVPKLLIYAAS					
CR2-1.45_LC	(1)	DIQMTQSP PSLS ASVGD RV TINCRASQGISNDLAWYQKPGKVPKLLIYAAS					
Consensus	(1)	DIQMTQSP PSLS ASVGD RV TI CRASQGISN LAWYQKPGKVPKLLIYAAS					
							Section 2
	(54)	60	70	80	90	106	
A20	(54)	LQSGVPSRFS SGSG SGTD FTLT ISSLOPEDVATYYCQRYNSAP-----					
CR2-1.45_LC	(54)	LQLGVPSRFS SGSG SGTD FTLT ISSLOPEDVATYYCQRYNSAPFTFGPGTKVDI					
Consensus	(54)	LQGVPSRFS SGSG SGTD FTLT ISSLOPEDVATYYCQRYNSAP					
							Section 3
	(107)						
A20	(96)	-					
CR2-1.45_LC	(107)	K					
Consensus	(107)						



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FIGURE 36

Figure 36A

		Section 1					
		(1)	1	10	20	30	40 51
VH1-8	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVROATGQGLEWMGWM					
CR2-1.46.1_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVROATGQGLEWMGWM					
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVROATGQGLEWMGWM					
		Section 2					
		(52)	52	60	70	80	90 102
VH1-8	(52)	NPNSGNTGYAQKFGGRVTMTNTSISTAYMELSSLRSEDTAVYYCAR----					
CR2-1.46.1_HC	(52)	NPNNENTGYAQKFGGRVTMTNTSISTAYMELSSLRSEDTAVYYCARDIVV					
Consensus	(52)	NPN GNTGYAQKFGGRVTMTNTSISTAYMELSSLRSEDTAVYYCAR					
		Section 3					
		(103)	103	110	126		
VH1-8	(99)	-----				SEQ ID NO:1	
CR2-1.46.1_HC	(103)	VVTATDYYYGMDVWGQGTTVTVSS				SEQ ID NO:40	
Consensus	(103)						

Figure 36B

		Section 1					
		(1)	1	10	20	30	40 52
A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLGWYQKPKGKPKRLITAAAS					
CR2-1.46.1_LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLGWYQKPKGKPKRLITAAAS					
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLGWYQKPKGKPKRLITAAAS					
		Section 2					
		(53)	53	60	70	80	90 104
A30	(53)	SLPSSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYP-----					
CR2-1.46.1_LC	(53)	SLPSSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSGYPPPTFGQGTKV					
Consensus	(53)	SL SGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOH YP					
		Section 3					
		(105)	1057				
A30	(96)	---				SEQ ID NO:11	
CR2-1.46.1_LC	(105)	EIK				SEQ ID NO:41	
Consensus	(105)						



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FIGURE 37

Figure 37A

		Section 1				
		(1)	1	10	20	30 40 51
CR2-1.48.1_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVROAPGGGLEWMGWI				
VH1-18	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVROAPGGGLEWMGWI				
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVROAPGGGLEWMGWI				
		Section 2				
		(52)	52	60	70	80 90 102
CR2-1.48.1_HC	(52)	SAYNGNTNYAQRLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDVEY				
VH1-18	(52)	SAYNGNTNYAQRLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR----				
Consensus	(52)	SAYNGNTNYAQRLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR				
		Section 3				
		(103)	103	110	125	
CR2-1.48.1_HC	(103)	YYDGSGLYYFDYWGQGLVTVSS				SEQ ID NO:42
VH1-18	(99)	-----				SEQ ID NO:2
Consensus	(103)					

Figure 37B

		Section 1				
		(1)	1	10	20	30 40 52
CR2-1.48.1_LC	(1)	DIQMTQSPSSVSASVGDRVTITCRASQGISWLAHWYQKPKAPKLLIYAAS				
L5	(1)	DIQMTQSPSSVSASVGDRVTITCRASQGISWLAHWYQKPKAPKLLIYAAS				
Consensus	(1)	DIQMTQSPSSVSASVGDRVTITCRASQGISWLAHWYQKPKAPKLLIYAAS				
		Section 2				
		(53)	53	60	70	80 90 104
CR2-1.48.1_LC	(53)	ILQSGVPSRFSGSGSGTDFTLTISSLQPEDFAFYCQQNSFPRTFGQGTKV				
L5	(53)	SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAFYCQQNSFP-----				
Consensus	(53)	LQSGVPSRFSGSGSGTDFTLTISSLQPEDFAFYCQQANSFP				
		Section 3				
		(105)	1057			
CR2-1.48.1_LC	(105)	EIK				SEQ ID NO:43
L5	(96)	---				SEQ ID NO:7
Consensus	(105)					

			<u>Section 1</u>					
	(1)	1	10	20	30	40	52	
CR2-1.49.1 LC	(1)	DIVMTQSPFLSLEVTPEGPASISCRSSQSLLHNSNGYNYLDWYLKPGQSPQLL						
A19	(1)	DIVMTQSPFLSTPVTPEGPASISCRSSQSLLHNSNGYNYLDWYLKPGQSPQLL						
Consensus	(1)	DIVMTQSPFLSLPVTPEGPASISCRSSQSLLHNSNGYNYLDWYL KPGQSPQLL						
			<u>Section 2</u>					
	(53)	53	60	70	80	90	104	
CR2-1.49.1 LC	(53)	IYLGSSRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQTLOTITFGQ						
A19	(53)	IYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMAQLQTPT---						
Consensus	(53)	IYLGSRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQ LQT						
			<u>Section 3</u>					
	(105)	105	111					
CR2-1.49.1 LC	(105)	GTRLEIK	SEQ ID NO:45					
A19	(101)	-----	SEQ ID NO:8					
Consensus	(105)							

Section 1

	(1)	10	20	30	40	52
CR2-1.51.1_LC	(1)	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLITYGA				
A27	(1)	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLITYGA				
Consensus	(1)	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLITYGA				

Section 2

	(53)	60	70	80	90	104
CR2-1.51.1_LC	(53)	SNRATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQYGSSLTPFGPGTK				
A27	(53)	SSRATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQYGSSP-----				
Consensus	(53)	S RATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQYGS				

Section 3

	(105)	10908
CR2-1.51.1_LC	(105)	VDIK
A27	(97)	----
Consensus	(105)	

SEQ ID NO:47

SEQ ID NO:10



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FIGURE 40

Figure 40A

								Section 1	
	(1)	1	10	20	30	40	52		
Cur2-6.4.1 hc	(1)	QVQLVQSGAEVRKFGASVKVSCRASGYTFTSYDINWVRQATGQGLEWMGWIN							IN
VH1-8	(1)	QVQLVQSGAEVRKFGASVKVSCRASGYTFTSYDINWVRQATGQGLEMMGWIN							IN
Consensus	(1)	QVQLVQSGAEVRKFGASVKVSCRASGYTFTSYDINWVRQATGQGLEWMGWIN							
								Section 2	
	(53)	53	60	70	80	90	104		
Cur2-6.4.1 hc	(53)	PNSGNTDYAQRKFGGRVTMTRDTSISTAYMELSSLRSEDTA						YYCVRGFGYSY	
VH1-8	(53)	PNSGNTGYAQRKFGGRVTMTRNTSISTAYMELSSLRSEDTA						YYCAR-----	
Consensus	(53)	PNSGNT YAQRKFGGRVTMTR TSISTAYMELSSLRSEDTAIYYC R							
								Section 3	
	(105)	105	110	125					
Cur2-6.4.1 hc	(105)	NYDYVYGMVWVGQGTTVTVSS			SEQ ID NO:48				
VH1-8	(99)	-----			SEQ ID NO:1				
Consensus	(105)								

Figure 40B

								Section 1
	(1)	1	10	20	30	40	52	
Cur2-6.4.1 Lc	(1)	EIVLTQSPGTL SLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLITY						T
A27	(1)	EIVLTQSPGTL SLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLITY						SA
Consensus	(1)	EIVLTQSPGTL SLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLIYA						
								Section 2
	(53)	53	60	70	80	90	104	
Cur2-6.4.1 Lc	(53)	SSRATGIPDRFSGSGSGTD FTLTISRLEPEDFAVYYCQYGSSECSFGQGTK						
A27	(53)	SSRATGIPDRFSGSGSGTD FTLTISRLEPEDFAVYYCQYGSSE-----						
Consensus	(53)	SSRATGIPDRFSGSGSGTD FTLTISRLEPEDFAVYYCQYGSSE						
								Section 3
	(105)	105	108					
Cur2-6.4.1 Lc	(105)	LEIK		SEQ ID NO:49				
A27	(97)	----		SEQ ID NO:10				
Consensus	(105)							